

#32 1644



1600

ENTERED

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/424,705B

DATE: 12/31/2002

TIME: 14:07:02

Input Set : A:\EP.txt

Output Set: N:\CRF4\12312002\I424705B.raw

RECEIVED

JAN 03 2003

TECH CENTER 1600/2900

```

4 <110> APPLICANT: LITTLE, MELVYN
5 KIPRIYANOV, SERGEY
6 MOLDENHAUER, GERHARD
7 DEUTSCHES KREBSFORSCHUNGSZEUTRUM
9 <120> TITLE OF INVENTION: MUTATED OKT3 ANTIBODY
12 <130> FILE REFERENCE: 035280047US00
14 <140> CURRENT APPLICATION NUMBER: 09/424,705B
15 <141> CURRENT FILING DATE: 2000-06-02
17 <150> PRIOR APPLICATION NUMBER: PCT/DE98/01409
18 <151> PRIOR FILING DATE: 1998-05-22
20 <160> NUMBER OF SEQ ID NOS: 11
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 909
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (28)...(900)
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35                               Met Lys Tyr Leu Leu Pro Thr Ala Ala
36                               1           5
38 gct ggc ttg ctg ctg ctg gca gct cag ccg gcc atg gcg cag gtg cag      102
39 Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln
40 10           15           20           25
42 ctg cag cag tct ggg gct gaa ctg gca aga cct ggg gcc tca gtg aag      150
43 Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys
44           30           35           40
46 atg tcc tgc aag gct tct ggc tac acc ttt act agg tac acg atg cac      198
47 Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
48           45           50           55
50 tgg gta aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att      246
51 Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile
52           60           65           70
54 aat cct agc cgt ggt tat act aat tac aat cag aag ttc aag gac aag      294
55 Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys
56           75           80           85
58 gcc aca ttg act aca gac aaa tcc tcc agc aca gcc tac atg caa ctg      342
59 Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu
60 90           95           100           105
62 agc agc ctg aca tct gag gac tct gca gtc tat tac tgt gca aga tat      390
63 Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr

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64          110          115          120
66 tat gat gat cat tac agc ctt gac tac tgg ggc caa ggc acc act ctc      438
67 Tyr Asp Asp His Tyr Ser Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu
68          125          130          135
70 aca gtc tcc tca gcc aaa aca aca ccc aag ctt gaa gaa ggt gaa ttt      486
71 Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu Glu Glu Gly Glu Phe
72          140          145          150
74 tca gaa gca cgc gta gat atc gtg ctc act cag tct cca gca atc atg      534
75 Ser Glu Ala Arg Val Asp Ile Val Leu Thr Gln Ser Pro Ala Ile Met
76          155          160          165
78 tct gca tct cca ggg gag aag gtc acc atg acc tgc agt gcc agc tca      582
79 Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser
80 170          175          180          185
82 agt gta agt tac atg aac tgg tac cag cag aag tca ggc acc tcc ccc      630
83 Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro
84          190          195          200
86 aaa aga tgg att tat gac aca tcc aaa ctg gct tct gga gtc cct gct      678
87 Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala
88          205          210          215
90 cac ttc agg ggc agt ggg tct ggg acc tct tac tct ctc aca atc agc      726
91 His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
92          220          225          230
94 ggc atg gag gct gaa gat gct gcc act tat tac tgc cag cag tgg agt      774
95 Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser
96          235          240          245
98 agt aac cca ttc acg ttc ggc tcg ggg aca aag ttg gaa ata aac cgg      822
99 Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asn Arg
100 250          255          260          265
102 gct gat act gca cca act gga tcc gaa caa aag ctg atc tca gaa gaa      870
103 Ala Asp Thr Ala Pro Thr Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu
104          270          275          280
106 gac cta aac tca cat cac cat cac cat cac taatctaga      909
107 Asp Leu Asn Ser His His His His His His
108          285          290
111 <210> SEQ ID NO: 2
112 <211> LENGTH: 291
113 <212> TYPE: PRT
114 <213> ORGANISM: Homo sapiens
116 <400> SEQUENCE: 2
117 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
118 1 5 10 15
119 Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
120 20 25 30
121 Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
122 35 40 45
123 Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
124 50 55 60
125 Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
126 65 70 75 80

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127 Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys
128      85      90      95
129 Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
130      100     105     110
131 Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Ser Leu
132      115     120     125
133 Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr
134      130     135     140
135 Thr Pro Lys Leu Glu Glu Gly Glu Phe Ser Glu Ala Arg Val Asp Ile
136 145      150     155     160
137 Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys
138      165     170     175
139 Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
140      180     185     190
141 Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr
142      195     200     205
143 Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser
144      210     215     220
145 Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala
146 225      230     235     240
147 Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly
148      245     250     255
149 Ser Gly Thr Lys Leu Glu Ile Asn Arg Ala Asp Thr Ala Pro Thr Gly
150      260     265     270
151 Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser His His His
152      275     280     285
153 His His His
154      290
156 <210> SEQ ID NO: 3
157 <211> LENGTH: 906
158 <212> TYPE: DNA
159 <213> ORGANISM: Homo sapiens
161 <220> FEATURE:
162 <221> NAME/KEY: CDS
163 <222> LOCATION: (28)...(897)
165 <400> SEQUENCE: 3
166 gaattcatta aagaggagaa attaacc atg aaa tac cta ttg cct acg gca gcc      54
167      Met Lys Tyr Leu Leu Pro Thr Ala Ala
168      1      5
170 gct ggc ttg ctg ctg ctg gca gct cag ccg gcc atg gcg cag gtg cag      102
171 Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln
172 10      15      20      25
174 ctg cag cag tct ggg gct gaa ctg gca aga cct ggg gcc tca gtg aag      150
175 Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys
176      30      35      40
178 atg.tcc tgc aag gct tct ggc tac acc ttt act agg tac acg atg cac      198
179 Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
180      45      50      55
182 tgg gta aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att      246

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```

183 Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile
184          60          65          70
186 aat cct agc cgt ggt tat act aat tac aat cag aag ttc aag gac aag      294
187 Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys
188          75          80          85
190 gac aag gcc aca ttg act aca gac aaa tcc tcc agc aca gcc tac atg      342
191 Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met
192 90          95          100          105
194 caa ctg agc agc ctg aca tct gag gac tct gca gtc tat tac tgt gca      390
195 Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
196          110          115          120
198 aga tat tat gat gat cat tac agc ctt gac tac tgg ggc caa ggc acc      438
199 Arg Tyr Tyr Asp Asp His Tyr Ser Leu Asp Tyr Trp Gly Gln Gly Thr
200          125          130          135
202 act ctc aca gtc tcc tca gcc aaa aca aca ccc aag ctt ggc ggt gat      486
203 Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu Gly Gly Asp
204          140          145          150
206 atc ttg ctc acc caa act cca gct tct ttg gct gtg tct cta ggg cag      534
207 Ile Leu Leu Thr Gln Thr Pro Ala Ser Leu Ala Val Ser Leu Gly Gln
208          155          160          165
210 agg gcc acc atc tcc tgc aag gcc agc caa agt gtt gat tat gat ggt      582
211 Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly
212 170          175          180          185
214 gat agt tat ttg aac tgg tac caa cag att cca gga cag cca ccc aaa      630
215 Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys
216          190          195          200
218 ctc ctc atc tat gat gca tcc aat cta gtt tct ggg atc cca ccc agg      678
219 Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg
220          205          210          215
222 ttt agt ggc agt ggg tct ggg aca gac ttc acc ctc aac atc cat cct      726
223 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro
224          220          225          230
226 gtg gag aag gtg gat gct gca acc tat cac tgt cag caa agt act gag      774
227 Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu
228          235          240          245
230 gat ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa cgg gct      822
231 Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala
232 250          255          260          265
234 gat gct gcg gcc gct gga tcc gaa caa aag ctg atc tca gaa gaa gac      870
235 Asp Ala Ala Ala Ala Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp
236          270          275          280
238 cta aac tca cat cac cat cac cat cac taaagatct      906
239 Leu Asn Ser His His His His His His
240          285          290
243 <210> SEQ ID NO: 4
244 <211> LENGTH: 290
245 <212> TYPE: PRT
246 <213> ORGANISM: Homo sapiens
248 <400> SEQUENCE: 4

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Input Set : A:\EP.txt

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```

249 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
250 1 5 10 15
251 Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
252 20 25 30
253 Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
254 35 40 45
255 Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
256 50 55 60
257 Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
258 65 70 75 80
259 Asn Tyr Asn Gln Lys Phe Lys Asp Lys Asp Lys Ala Thr Leu Thr Thr
260 85 90 95
261 Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser
262 100 105 110
263 Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr
264 115 120 125
265 Ser Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala
266 130 135 140
267 Lys Thr Thr Pro Lys Leu Gly Gly Asp Ile Leu Leu Thr Gln Thr Pro
268 145 150 155 160
269 Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys
270 165 170 175
271 Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr
272 180 185 190
273 Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser
274 195 200 205
275 Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly
276 210 215 220
277 Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala
278 225 230 235 240
279 Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly
280 245 250 255
281 Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Ala Ala Gly Ser
282 260 265 270
283 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser His His His His
284 275 280 285
285 His His
286 290
288 <210> SEQ ID NO: 5
289 <211> LENGTH: 900
290 <212> TYPE: DNA
291 <213> ORGANISM: Homo sapiens
293 <220> FEATURE:
294 <221> NAME/KEY: CDS
295 <222> LOCATION: (28)...(891)
297 <400> SEQUENCE: 5
298 agatctatta aagaggagaa attaacc atg aaa tac cta ttg cct acg gca gcc 54
299 Met Lys Tyr Leu Leu Pro Thr Ala Ala
300 1 5

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VERIFICATION SUMMARY

DATE: 12/31/2002

PATENT APPLICATION: **US/09/424,705B**

TIME: 14:07:03

Input Set : **A:\EP.txt**

Output Set: **N:\CRF4\12312002\I424705B.raw**